

Suppressor Genes of Conditional *TIF51A* Mutants that Produce Stable eIF5A

Watanabe, T.F.; Nogueira, M.A.; Rossi, D.; Dias, C.A.O.; Zanelli, C.F. & Valentini, S.R.

Departamento de Ciências Biológicas, Faculdade de Ciências Farmacêuticas,
Universidade Estadual Paulista, Araraquara, Brazil

The translation initiation factor 5A (eIF5A) is highly conserved from archaea to mammals, essential for cell viability and is the only protein known to contain the amino acid hypusine. In *Saccharomyces cerevisiae*, eIF5A is encoded by *TIF51A* under aerobic conditions. Structure and function studies of eIF5A performed in our laboratory generated two new conditional alleles of *TIF51A*, *tif51A*^{K56A} and *tif51A*^{Q22H/L93F}, which produce stable eIF5A at the restrictive temperature. Here, we describe the search for genes that allow growth of the conditional mutants eIF5A^{K56A} and eIF5A^{Q22H/L93F} at the restrictive temperature when present in high-copy number. This study might uncover factors that re-establish the lack of function due to loss of specific physical interactions. Using *tif51A*^{Q22H/L93F}, 7.5x10⁵ transformants were screened, out of which 731 grew at the restrictive temperature. So far, 531 candidates were analysed and three clones were confirmed by plasmid linkage. DNA sequencing of high-copy suppressor plasmid identified *TIF51A*, as expected, and a new suppressor, a tRNA gene. Although eIF5A was originally identified as a translation initiation factor, subsequent data such as a reduction of polysome run off and an increase of the average ribosome transit time of an eIF5A mutant have supported a function for eIF5A in the elongation step of protein synthesis. The new *TIF51A* mutant suppressor described here (tRNA gene) and other genes that may be revealed in the suppressor screening might be useful in the elucidation of the cellular mechanism played by eIF5A in translation.

Keywords: eIF5A, *Saccharomyces cerevisiae*, suppressor Genes
Supported by FAPESP, CNPq and CAPES